SEQUENCE LISTING

<110> Schnorr, Kirk Matthew
Christensen, Lars Lehmann Hylling

<120> Fungal carbohydrate-binding module

<130> 10499.204-US

<160> 9

<170> PatentIn version 3.3

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<221> CDS
<222> (10)..(531)

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att gga gct gcc aat gcc cac act cgt gtc tac gga ctc tcc gtc aac      99
Ile Gly Ala Ala Asn Ala His Thr Arg Val Tyr Gly Leu Ser Val Asn
15                  20                  25                  30

gat gtc aca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc     147
Asp Val Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser
                35                  40                  45

agt att gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt     195
Ser Ile Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val
            50                  55                  60

cag gtc cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc     243
Gln Val Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr
        65                  70                  75

gac atc cct act ttc act gct act gat gtt cct atc ttc acc aag aag     291
Asp Ile Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys
    80                  85                  90

ccc caa cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct     339
Pro Gln Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser
95                  100                 105                 110

gtt tca ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg     387
Val Ser Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala
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Ser Thr Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys
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Leu Asp Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly
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gga gtt gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat      531
Gly Val Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
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gtaggggagg tgagatggag taagattaag cggccgca                            629


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Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
        35                  40                  45


Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
    50                  55                  60


Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
65                  70                  75                  80


Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
                85                  90                  95


Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
            100                 105                 110


Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
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Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
    130                 135                 140
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<223> Positions 1-57 Candida lipase signal peptide, positions 58-147 Candida lipase sequence, positions 148-570 P. nigrella CBM polypeptide.

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gtt gca gcc act cct ttg gtg aag tgc gca act agt ggc cat tac ggc 96
Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly
20 25 30

ctc gcg agg ccg cct cgg ccc caa cga att ctt gga ata tta agc ttt 144
Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe
35 40 45

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tca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc agt att      192
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    50                  55                  60

gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt cag gtc      240
Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
65                  70                  75                  80

cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc gac atc      288
Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
                85                  90                  95

cct act ttc act gct act gat gtt cct atc ttc acc aag aag ccc caa      336
Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
            100                 105                 110

cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct gtt tca      384
Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
        115                 120                 125

ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg agc aca      432
Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
    130                 135                 140

atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc ctt gac      480
Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
145                 150                 155                 160

gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga gga gtt      528
Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
                165                 170                 175

gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat tag          573
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Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe
        35                  40                  45
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Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
    50                  55                  60

Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
65                  70                  75                  80

Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
                85                  90                  95

Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
            100                 105                 110

Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
        115                 120                 125

Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
    130                 135                 140

Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
145                 150                 155                 160

Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
                165                 170                 175

Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
            180                 185                 190
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